

S1 Table. High-throughput cloning of cellulase and other carbohydrate-active enzyme genes.

Reaction ID	Species	Family	Fragment size (bp) ^a	Colonies per transformation ^b	Correct band in colony PCR	Issues with PCR?
1	<i>Talaromyces emersonii</i>	GH6	1411	18	2/3	multiple bands
2	<i>Neurospora crassa</i>	AA9	769	45	3/3	smear
3	<i>Thermobifida fusca</i>	AA10	658	31	1/1	-
4	<i>Chrysosporium lucknowense</i>	GH7	1282	54	2/3	multiple bands
5	<i>Acidothermus cellulolyticus</i>	GH12	769	100	1/1	-
6	<i>Chaetomium thermophilum</i>	GH7	1456	35	1/3	multiple bands
7	<i>Neosartorya fischeri</i>	GH7	1456	43	1/1	multiple bands
8	<i>Clostridium termitidis</i>	GH8	1216	56	1/1	-
9	<i>Gibberella zeae</i>	GH45	1003	125	1/1	-
10	<i>Trichoderma viride</i>	GH5	1357	130	1/1	-
11	<i>Paenibacillus barcinonensis</i>	GH5	1201	112	1/1	-
12	<i>Talaromyces stipitatus</i>	GH5	1063	87	1/1	multiple bands
13	<i>Talaromyces cellulolyticus</i>	GH6	1201	69	3/3	multiple bands
14	<i>Talaromyces marneffeii</i>	GH7	1435	65	1/1	-
15	<i>Saccharophagus degradans</i>	GH5	943	42	1/1	-
16	Uncultured organism	GH5	1024	80	1/1	-
17	<i>Aureobasidium pullulans</i>	GH5	1000	24	2/2	multiple bands
18	<i>Trichoderma koningii</i>	GH6	1162	14	2/2	-
19	<i>Cytophaga hutchinsonii</i>	GH5	913	30	2/2	-
20	<i>Trichoderma koningii</i>	GH12	754	11	2/2	-
21	Uncultured organism	GH5	997	5	2/2	-
22	<i>Thielavia terrestris</i>	GH7	1459	5	1/2	multiple bands
23	<i>Myceliophthora thermophila</i>	GH5	985	16	2/2	-
24	<i>Thielavia terrestris</i>	GH1	1525	16	2/2	-
25	<i>Thielavia terrestris</i>	GH6	1189	25	2/2	-
26	<i>Trichoderma reesei</i> ^c	GH6	1447	8	1/2	multiple bands
27	<i>Trichoderma reesei</i>	GH6	1447	19	2/2	-
28	<i>Trichoderma reesei</i> ^c	GH5	1297	24	3/3	-
29	<i>Trichoderma reesei</i>	GH5	1297	4	2/3	-

^a All fragments contained 40 bp of overlapping sequences with the vector at each end; coding sequences were codon-optimized using a published algorithm (Lanza et al., 2014), synthesized with BioXp™ 3200 (SGI-DNA), and PCR-amplified with PrimeSTAR Max polymerase (Takara Bio).

^b 5 ng of a 7-kb custom vector was cotransformed with 5 ng insert, giving molar insert-to-vector ratio between 5:1 and 9:1.

^c Native rather than codon-optimized cellulase sequences were used in these reactions.